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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2003, 09:42:00 : Search time 13 seconds

(without alignments)
2.368 Million cell updates/sec

Title: us-09-872-523-5
Perfect score: 2656
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Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1 segs, 30911 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
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Database : 19-apr-1996-z71266.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	2520.5	94.9	30911	1 CER06C7	ALIGNMENTS ACCESSION:Z71266

ALIGNMENTS

RESULT 1
CER06C7/c CER06C7 30911 bp DNA linear INV 19-APR-1996
LOCUS Caenorhabditis elegans cosmid R06C7.
DEFINITION
ACCESSION Z71266
VERSION 271266 GI:1279324
KEYWORDS adenylsuccinate lyase, myosin heavy chain, Rat TOAD-64 protein
like, serine/threonine-protein kinase, zinc finger protein.
SOURCE
ORGANISM Caenorhabditis elegans
Eukaryote; mitochondrial eukaryotes; Metazoa; Nematoda;
Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
REFERENCE
1 (bases 1 to 30911)
Gardner, A.
TITLE Direct Submission

JOURNAL

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
COMMENTFEATURES
SOURCE

CDS

CDS

Submitted (19-APR-1996) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or twenematode.wustl.edu
2 (bases 1 to 30911)
Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
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Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
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Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J. and Wohldman, P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
Nature 368 (6466), 32-38 (1994)
94150718
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
clone R06C7. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
The true left end of clone R06C7 is at 1 in this sequence. The true
left end of clone F21c3 is at 30808 in this sequence. Coding the
sequences below are predicted from computer analysis, using the
program GeneFINDER (P. Green, ms in preparation), and other
available information.
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sequence CEP21C3.
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comes from this gene; cDNA EST yk93h1.5 comes from this
gene; cDNA EST yk1344.5 comes from this gene; cDNA EST
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from this gene; cDNA EST yk25b2.3 comes from this gene;
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QY      116 ----- 116
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Search completed: October 28, 2003, 09:42:20
Job time : 19 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 28, 2003, 09:45:58 ; Search time 24 Seconds

(without alignments)
3.856 Million cell updates/sec

Title: us-09-872-523-6

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Scoring table:

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Searched: 1 seqs, 30911 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Database : 19-apr-1996-271266.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Z71266 GI:1279324
adenylosuccinate lyase; myosin heavy chain; Rat TOAD-64 protein like; serine/threonine-protein kinase; zinc finger protein.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryotes; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.
1 (bases 1 to 30911)
Gardner, A.

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (19-Apr-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RO, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jee@sanger.ac.uk or tw@nemacode.wustl.edu
2 (bases 1 to 30911)
Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copestake, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kerhaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,

JOURNAL
MEDLINE
COMMENT

FEATURES

source

CDS

CDS

O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Showken, R., Smalton, N., Smith, A., Sonhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterson, R., Watson, A., Weinstein, L., Wilkinson-Sproat, J., and Wohlman, P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans
Nature 368 (6466), 32-38 (1994)
94150718
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of clone R06C7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring subclones.
The true left end of clone R06C7 is at 1 in this sequence. The true left end of clone P21C3 is at 30808 in this sequence. Coding sequences below are predicted from computer analysis, using the program GeneFINDER (P. Green, ms in preparation), and other available information.
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CEP21C3.
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 28, 2003, 09:42:00 ; Search time 13 Seconds

(without alignments)
2.368 Million cell updates/sec

Title: us-09-872-523-5

Perfect score: 2656

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Scoring table: BLOSUM62

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Ygapop 10.0	Ygapext 0.5
Dgapop 6.0	Dgapext 7.0
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Searched: 1 seqs, 30911 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 1 summaries

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Database: 19-apr-1996-271266:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	2520.5	94.9	30911	1 CER06C7	ALIGNMENTS ACCESSION:271266

ALIGNMENTS

RESULT 1
CER06C7/c
LOCUS CER06C7
DEFINITION Caenorhabditis elegans cosmid R06C7.
ACCESSION 271266
VERSION 271266
KEYWORDS GI:1279324
adenylosuccinate lyase; myosin heavy chain; Rat TOAD-64 protein
like; serine/threonine-protein kinase; zinc finger protein.
SOURCE Caenorhabditis elegans
ORGANISM Caenorhabditis elegans

REFERENCE 1
AUTHORS Rhabditidae; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Gardner, A.
TITLE Direct Submission

JOURNAL

Submitted (19-Apr-1996) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or tw@nematode.wustl.edu

REFERENCE

2 (bases 1 to 30911)
Wilson, R., Almscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkes, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kersey, J., Kirsten, U., Latreille, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rinken, L., Roopra, A.,
Saunders, D., Showkeen, R., Smaford, N., Smith, A., Sonhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J., and Wohlman, P.

TITLE

JOURNAL

MEDLINE

COMMENT

Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of
clone R06C7. It may be shorter because we only arrange for a small
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.

The true left end of clone R06C7 is at 1 in this sequence. The true
left end of clone F21C3 is at 30808 in this sequence. Coding
sequences below are predicted from computer analysis, using the
program GeneFinder (P. Green, ms in preparation), and other
available information.

The end of this sequence (30808..30911) overlaps with the start of
sequence CEF21C3.

FEATURES

source

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Best Local Similarity: 80.75% Mismatches: 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
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Searched: 1 segs, 30911 residues

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Listing first 1 summaries

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SUMMARIES

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ALIGNMENTS

RESULT 1
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1 (bases 1 to 30911)
Gardner, A.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (19-APR-1996) Nematode Sequencing Project, Sanger Centre,
JOURNAL Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail: jess@anger.ac.uk or tw@nematode.wustl.edu
2 (bases 1 to 30911)
Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, J., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,

TITLE
JOURNAL
MEDLINE
COMMENT
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Showken, R., Smailon, N., Smith, A., Sonhammer, E., Staden, R., Sulten, J., Thierry-Mieg, J., Thoms, K., Vautin, M., Vaughan, K., Waterton, R., Watson, A., Weinstock, L., Wilkinson-Sprat, J., and Wohlman, P.
2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans
Nature 368 (6466), 32-38 (1994)

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of clone R06C7. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
The true left end of clone R06C7 is at 1 in this sequence. The true left end of clone F21C3 is at 30808 in this sequence. Coding sequences below are predicted from computer analysis, using the program GeneFinder (P. Green, ms in preparation), and other available information.
The end of this sequence (30808..30911) overlaps with the start of sequence CEF21C3.

FEATURES

source

CDS

CDS

Location/Qualifiers
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CDS
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